

GenCore version 4.5
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OM Protein - Protein search, using sw model

Run on: July 18, 2001, 15:56:47 ; Search time 19.26 Seconds

(without alignments)
3021.670 Million cell updates/sec

Title: US-09-587-111-5
Perfect score: 4004
Sequence: 1 MTSPPSSPVFVLETLDDGQE EDEDGASEENYVPVQLLQSN 764
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-68:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	RESULT	1
1	1652	41.3	838	2 T09054	T09054	capsaicin receptor - rat
2	634	15.8	725	3 JG7531	Qy	18 GQEDGEADRKQLDFGSGLPPMMESSOFOGEDERKFAQIRVN--LNRYKGTG-----
3	414	10.3	900	2 T33026	Db	51 GKGDSFEAS-----PLDCYEEGLASCLPITVSSVLTQRPDGAPASVRPSSQ 99
4	392	9.8	790	2 T20312	Qy	66 ---ASQDPNPRFDRLRNLAVNSRGVPEDLAGLPBLVSKYLTSDSEYVGSTGKTCM 121
5	364	9.1	937	2 T37241	Db	100 DSVSAGEKPPPLYDRRSIFDAVAQSNQCELESLLPFLORSKKRKLTDSEFRDPETGKTCIL 159
6	261	6.5	519	2 T24772	Qy	122 KAVLNLDGVNACTIPLQDSDCNPQVINAQCTDDYRGHSAHLIAEKRSLOCVKL 181
7	209	5.2	1188	2 T19552	Db	160 KAMLNLLHNGQNTIALLDYARKTDSLKFVNAASYTDSYYKGQTAHLAERRNMTLV 219
8	197.5	4.9	1124	2 JH0588	Qy	182 LVENGANVHARRACGRGFQKOGG-TCFYFGELPLSLACRQWDVSYLLENPHOPASLQA 240
9	191	4.8	1274	2 JH0015	Db	220 LVENGADVOAAANGPFKKKGRCFYPFEGELPLSLACQNQLAIVKFLQNSKOPADSA 279
10	190.5	4.8	1275	2 JH0092	Qy	301 AAKEGKTEIRHTILOREF--SGLSLHSRKTEWCYGPVRLSYLDSLAVSCEENSYLETT 358
11	174	4.3	810	2 T38361	Db	341 TDSOGNVLVHALVMDSNABNIALVTSMYDGLQAGARLCPVQLEDTRNLQDILPLK 300
12	167.5	4.2	934	1 H1274	Qy	340 KASGKIGVLYLIOREIHEPECRHLSRKTEWAXGPVHSSLYLDSCIPCEKNVLEVI 399
13	157	3.9	481	2 T23729	Db	359 AF-HOKSPHRMRMVYLEPLKLUQKWLDPK-FFLNLCLNLYMFETAVAYHQPLK 416
14	157	3.9	1549	2 T13940	Qy	359 AF-HOKSPHRMRMVYLEPLKLUQKWLDPK-FFLNLCLNLYMFETAVAYHQPLK 416
15	151	3.8	1765	2 T42714	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
16	151	3.8	1940	2 T42715	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
17	151	3.8	1943	2 T42713	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
18	151	3.8	1961	2 T42716	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
19	151	3.8	3924	2 S37431	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
20	150.5	3.8	793	2 S68238	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
21	150	3.7	887	2 T03939	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
22	150	3.7	A55575	2 ankyrin 3, splice	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
23	147	3.7	1001	2 S30385	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
24	143	3.6	842	2 T32258	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
25	141.5	3.5	683	2 A85044	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
26	140	3.5	1848	2 S33771	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
27	140	3.5	14502	2 I49502	Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
28	139.5	3.5	1411	2 S30355	Qy	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457
29	138	2	B35049		Db	400 AYSSETPNRIDMLIVEPLRLLQDKWDRKTFYFNFPVYCLWIMFTAAVYRPV-- 457

QY	376 LNKLIQAWKWDLILPK-FEFLNQLNLYWHEIFTAV------AYHQP-- 413
Db	409 LTDLLEAKWEFAKRNMIVSFTARTYLTYCFTAFLTRPFGSTEMLTAEWGWINRYSEPP 468
QY	414 -----TUKKOAP-----HLKAEVGNSMLTGHITLIGGYIILV 448
Db	469 GRGVKNSTLQQVPRVINATSRGLVIEWSPLSQCHLRNWDPDTPFANSYIRLPELFVII 528
QY	449 GOLWYFWRRHFWIWSID-----SYFEILEFQALIT-----WVSQLCFLATEW 494
Db	529 GIC-----VOVFLDFRDIKIGRKWWNVNLTAFFPAKATTEKLTYFLVAMIPRLACDL 581
QY	495 YPLLV-----SALVIGWLNLYYTRGFQHGIYSNIQKVYLDRDLRFLILYLVLF 547
Db	582 SPVLYWVNDNLVLTWMTFTVHLYCRVTFVGPFVLMVNTIATDIFRFMLIYGIFL 641
QY	548 GF-----AVALVLSQBAAWRPEAFTGPNTESQPMQED-----GNGAQY 590
Db	642 GFSQSFSLIFLSC-----RANVIKKLTDSEASESGSDMKFNLTROQISADTAVKNAEVF 699
QY	591 RGITLEASLELF---KFTIGMELAFEQELHFRGHLV-----LLLAVLTVILL 637
Db	700 ENVMOSPIEA弗VRUFLITGEFT---VLYRNALCPANTMWIGKVVFILFELFSINQ 755
QY	638 LNMLIALMSETVNSVATDWSWIWKLQKASVLEME 672
Db	756 FNMLLIAMMRTYETIFQTCLE-YKQRQAQVILMLE 789
RESULT	4
T20312	hypothetical protein F28H7.10 - <i>Caenorhabditis elegans</i>
C-Species:	<i>Caenorhabditis elegans</i>
C-Date:	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C-Accession:	T20312; T21533
A-Matthews, P.	submitted to the EMBL Data Library, June 1996
A-Reference number:	Z19255
A-Accession:	T20312
A-Status:	preliminary; translated from GB/EMBL/DDJB
A-Molecule type:	RNA
A-Residues:	1-1790 <WIL>
A-Cross-references:	EMBL:Z74030; PIDN:CAA98449_1; GSPDB:GN00023; CESP:F28H7.10
A-Experimental source:	clone D1054
A-Berks, M.	submitted to the EMBL Data Library, May 1996
A-Reference number:	Z19435
A-Accession:	T21533
A-Status:	preliminary; translated from GB/EMBL/DDJB
A-Molecule type:	DNA
A-Residues:	1-1790 <WIL>
A-Cross-references:	EMBL:Z72508; PIDN:CAA96644_1; GSPDB:GN00023; CESP:F28H7.10
A-Experimental source:	clone F28H7
C;Genetics:	
A;Gene:	CESP:F28H7.10
A;Map position:	5
A;Introns:	46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67
Query Match	9.8%; Score 392.5; DB 2; Length 790;
Best Local Similarity	25.3%; Pred. No. 2.6e-22; Indels 189; Gaps 35;
Matches	182; Conservative 106; Mismatches 243; Indels 189; Gaps 35;
QY	61 RKGTFASQPD-PNRFDRLRFNAVSRGVPPEDIAGLPEYLISKYLT-----TDSBYT 111
Db	101 KKGKGKGSQPNILDEFDOGQ-----AEMAG---DLKKALKLBDGGGGKSEKWR 147
QY	112 E-----GSQKT-----CLMR-----AVLNLKDGYNACIPLQIQLDRSGNP-----LVAQOC 156
Db	148 EMWWSVDERGSGMGENLIAICLQLGSALH-----TARRLINFFPKKLINDIC 194
QY	157 TDDYVRGHSALIATIERSLQCVKLUVENGANGHARACGRFF---OKGQGT-----204
QY	205 -----CFYFCFLPLSLAACTKQDWVSYLPHNPHOPLAQDATSGONTVHALVM 254
Db	255 ELTKKNTNTGSMYMFGEYPLSPAICMGHDLFMLA--KKANLSDQTNNTAL-H-LCV 310
QY	255 ISDNRAENIALVTSMDGLIQLQAGARLCPTVQLEDIRNLQDITPLKLAAK-EKIEIFRH 313
Db	311 IHDK-----MDMLDAVLEAGNNI-----RLANKQNTIALTIAARLAKKTSIQH 355
QY	314 LOREFGGLSH--LSRKFTEW-CYGPVRSVLSDA-SVDSCEENSVEITAHC----- 362
Db	356 --ELMPGLITQILDEK--RRAVY-----RALWRLSGLFIFYCCFCVAYML 398
QY	363 -----KSPHRHRMV-----LEPLNKLQAKWDLILPKFFNLQNLIMFIFTAVAHQ 412
Db	399 RPSSATTEHJTRGRINDDGETESTNSTNYLQWA-----IDTOCHHLMY--YSAWPWYH 449
QY	413 PTLKQOAPHLAEGVNSMLTGHITLILGCGIYLQMLWQFRRIWFNTSFIDSYFEI 472
Db	450 GWFR-----LGCEMTITIWLQFQILDFGDIRRGFQKF-----NFLKAPAK 493
QY	473 LFLFQALLTVVSVQVCFAL---EYVL-----PLMSALVIGWLNLYYTRGFQHGIYSV 525
Db	494 LMFKGAFLITIISICLACSFHFEPFLTDNTMAITISLTLQHFRYMAIPFVGPFV 553
QY	526 MIQKUILDRFLILYLVLFPGFVALVLSQEARPPEAFTGPNTESQPMQEDEG 585
Db	554 MVTIYTATDVRFAMYISLTVLFGESQSFYLFITSFERS-----PAIKKIDPM----- 601
QY	586 NGAQYRGILE---ASLELKFTINGELAFOE-----QHFRGAVLILLYAVIYIL 636
Db	602 -GSEFNINMENPVDALRIFTIMIGEFPSVLYREMASCDNFWMKWIGKLITVIFETFSIL 660
QY	637 LNMLIALMSETVNSVATDWSWIWKLQKASVLEME 696
Db	661 QFNLLIAMMRTYETIFL-TKREWTRQWADYVILMELMGUSPASRMH---LLRVTPTG 715
RESULT	5
T37241	olfactory channel protein osm-9 - <i>Caenorhabditis elegans</i>
C-Species:	<i>Caenorhabditis elegans</i>
C-Date:	03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C-Accession:	T37241
R;Covert, H.A.; Smith, T.L.; Bargmann, C.I.	J. Neurosci. 17, 8259-8269, 1997
A-Tittle:	OSM-9, A novel protein with structural similarity to channels, is required for
A-Reference number:	Z21659; NUID:9747745
A-Accession:	T37241
A-Status:	preliminary; translated from GB/EMBL/DDJB
A-Molecule type:	mRNA
A-Residues:	1-937 <COL>
A-Cross-references:	EMBL:AF031408; NID:92642589; PIDN:AAB87064_1; PID:92642590
C;Genetics:	
A;Gene:	osm-9
A;Map position:	IV
C;Keywords:	transmembrane protein
Query Match	9.1%; Score 364; DB 2; Length 937;
Best Local Similarity	23.9%; Pred. No. 5.4e-20; Matches 160; Conservative 101; Mismatches 254; Indels 154; Gaps 23;
Matches	160; Conservative 101; Mismatches 254; Indels 154; Gaps 23;
QY	98 LSKTKYLTSEYB-----GSTGTCIPLKAVLNKDGYNACIPLQIQLDRSGN 147
Db	103 LSESEVDMDQSPRHYKALWKLNGKEVEG-LHILLRERQCYCETIARL-IKRFPG- 159
QY	148 PQLVNAQCTDDYFGHSALIATEKRSLOCVKLUVENGANGHARACGRFF-----198
Db	160 ---MANDIVLGDEFGQSAHLATVHDYETVULLNSRADNARAGNFFLPDFKLIN 216
QY	199 --OKQOGTFCYFGEPLSLAECTKQDWVSYLPHNPHOPLAQDATSGONTVHALVM 254

QY 217 KTDYQGA-YYGEPYLFAACFGNKDITDILIOFGAND-NLQ--DSFENTILHMCV-- 269
 Db 217 KTDYQGA-YYGEPYLFAACFGNKDITDILIOFGAND-NLQ--DSFENTILHMCV-- 269
 QY 257 DNAENTALVTSMWDGLIQQAGARICPTVOLEDDIRNLQDTPLKLAKEKGKIEFRHILOR 316
 Db 257 DNAENTALVTSMWDGLIQQAGARICPTVOLEDDIRNLQDTPLKLAKEKGKIEFRHILOR 316
 QY 270 -----INWSSMSYAVRWAKPAD---PHVUNHAGTPIPLATKLGKRQTEEME- 318
 Db 270 -----INWSSMSYAVRWAKPAD---PHVUNHAGTPIPLATKLGKRQTEEME- 318
 QY 317 EFGSLSHSRKETEPCYGVRSVLASVDSC-----ENSELETIAFHCKSPHRHR 369
 Db 317 EFGSLSHSRKETEPCYGVRSVLASVDSC-----ENSELETIAFHCKSPHRHR 369
 QY 319 -----IMKVEFWRFSDMTCSAQNPLNLTIDTOPGSNYSALMTV- -NGSTPEHLD 368
 Db 319 -----IMKVEFWRFSDMTCSAQNPLNLTIDTOPGSNYSALMTV- -NGSTPEHLD 368
 QY 370 MUVLEPLNKLQKWDLIPKPEFLNFCNLQIYMPI-FTVAVYHOPTLKQOAPHKAEGV 428
 Db 370 MUVLEPLNKLQKWDLIPKPEFLNFCNLQIYMPI-FTVAVYHOPTLKQOAPHKAEGV 428
 QY 369 MIGSEVIIORLLADKWKAFQKRLIERLVLLIVOLITLSIVYIRPT---ELPRLYMEDP 424
 Db 369 MIGSEVIIORLLADKWKAFQKRLIERLVLLIVOLITLSIVYIRPT---ELPRLYMEDP 424
 QY 429 NSMLLTGHILLLGGIYLGVQLMWFWRRHFIWISFDISFEILFLFQLLTV---- 482
 Db 429 NSMLLTGHILLLGGIYLGVQLMWFWRRHFIWISFDISFEILFLFQLLTV---- 482
 QY 425 Q-----WDDYTRTACELLTILNCIFFVGQQLG 452
 Db 425 Q-----WDDYTRTACELLTILNCIFFVGQQLG 452
 QY 483 -----VSQVICFLATEWL-----PLVSLVALVGLNL 510
 Db 483 -----VSQVICFLATEWL-----PLVSLVALVGLNL 510
 QY 453 EIRTQGMGRGYLNRNKTAPAKAVFCIANFLFLCIPFLMKKHETEALNVFALPGSWIFL 512
 Db 453 EIRTQGMGRGYLNRNKTAPAKAVFCIANFLFLCIPFLMKKHETEALNVFALPGSWIFL 512
 QY 511 LYVTRGFQHTGIVSYVMQKVLIRDLLFLILYFLFGAVA--LVSLSQEARWPEAPT 568
 Db 511 LYVTRGFQHTGIVSYVMQKVLIRDLLFLILYFLFGAVA--LVSLSQEARWPEAPT 568
 QY 513 LEFFARSALKLTGPVOMIYMSIAGDMIRFAISAFLVFLHSQVFVFGKMDAKQKLEDTN 572
 Db 513 LEFFARSALKLTGPVOMIYMSIAGDMIRFAISAFLVFLHSQVFVFGKMDAKQKLEDTN 572
 QY 569 PNATESVOPMEGODEGNGAQYRGILENSLELFKFTIGELAFOEQLIFRGMVILLILA 628
 Db 569 PNATESVOPMEGODEGNGAQYRGILENSLELFKFTIGELAFOEQLIFRGMVILLILA 628
 QY 573 PHACR---ISGY---TITYNTFPETITLFRASMGYDYEESCANQAOALTTLFWL 624
 Db 573 PHACR---ISGY---TITYNTFPETITLFRASMGYDYEESCANQAOALTTLFWL 624
 QY 629 YVILTYILINLNMITALMBETVNSVATDSWSIWIQKA- ISVLMENGYWWCRKORAGV 686
 Db 629 YVILTYILINLNMITALMBETVNSVATDSWSIWIQKA- ISVLMENGYWWCRKORAGV 686
 QY 625 YMVFMPIMMINLJAMMGNYTTVIAQAEKAWROOQYAQIVMVLRSVG---KERLAAS 679
 Db 625 YMVFMPIMMINLJAMMGNYTTVIAQAEKAWROOQYAQIVMVLRSVG---KERLAAS 679
 QY 687 MLVVGTKD 695
 Db 680 QLEYSIRLD 688

RESULT 6

T24772 hypothetical protein T10B10.7 - Caenorhabditis elegans

C.Species: *Caenorhabditis elegans*
 C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T19552

R.Dobson, R.
 submitted to the EMBL Data Library, May 1996
 A;Reference number: Z19141

A;Accession: T19552

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1188 <WIL>

A;Cross-references: EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2

A;Experimental source: clone C29E6

C;Genetics:

A;Gene: CESP:C29E6.2

A;Map position: 4

A;Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match 5.2%; Score: 209; DB: 2; Length: 1188;
 Best Local Similarity 19.1%; Pred. No: 8.1e-08;
 Matches 152; Conservative 110; Mismatches 242; Gaps 39; Indels 290; Gaps 39;

QY 72 NRFFDRD--LENANVSRGPEDLAGPDEYLPSRTSKYLTDSLSETTEGSTGKTCLMKAVLNK 128
 Db 72 NRFFDRD--LENANVSRGPEDLAGPDEYLPSRTSKYLTDSLSETTEGSTGKTCLMKAVLNK 128
 QY 450 NMVRDONTPMHVAVSNGYLEMQLQOKHGASITQVNEDEE-----TALHRAIGVR 501
 Db 450 NMVRDONTPMHVAVSNGYLEMQLQOKHGASITQVNEDEE-----TALHRAIGVR 501
 QY 129 DGVNACTILPLQIIDDGSNPQPLVNAQCTDDYRGRHSALHIAEKRSLOCVKUENGAN 188
 Db 129 DGVNACTILPLQIIDDGSNPQPLVNAQCTDDYRGRHSALHIAEKRSLOCVKUENGAN 188
 QY 502 QLLEWDIIRLLMKDE-----MGNSALHLARRSGHDATTKVLLDNGAD 543
 Db 502 QLLEWDIIRLLMKDE-----MGNSALHLARRSGHDATTKVLLDNGAD 543
 QY 189 VHAR-----ACGRFFQKG-----QCTCFYFGELPLSLAA 217
 Db 189 VHAR-----ACGRFFQKG-----QCTCFYFGELPLSLAA 217
 QY 544 KEAKANSQKTPLOQAVDSGKLEMTCQVAKQAEIESSDTKTVLHTAAFYGN----- 596
 Db 544 KEAKANSQKTPLOQAVDSGKLEMTCQVAKQAEIESSDTKTVLHTAAFYGN----- 596
 QY 218 CTQKQDVYSLLENPHOPASLQATDSQNTVHLHALVMSDNAENIA--LVTSMYDGIL 274
 Db 218 CTQKQDVYSLLENPHOPASLQATDSQNTVHLHALVMSDNAENIA--LVTSMYDGIL 274
 QY 597 -----SIVRYFTA--EGYTIDRRDEGKT---AFDIACENDKKVARAFLETQWNLM 645
 Db 597 -----SIVRYFTA--EGYTIDRRDEGKT---AFDIACENDKKVARAFLETQWNLM 645
 QY 275 QAGARICPTVOLEDIR--NLQDTPLKLAKEKGKITEFRHILQREFSGLSHSRKFW 331
 Db 275 QAGARICPTVOLEDIR--NLQDTPLKLAKEKGKITEFRHILQREFSGLSHSRKFW 331
 QY 646 IP---CDVIVPLDKHRNPVNMRKRTP-----FRTLL-----TKFPE- 677
 Db 646 IP---CDVIVPLDKHRNPVNMRKRTP-----FRTLL-----TKFPE- 677
 QY 332 CYGPVRSVLYDLAS--VDSC-----EENSLEIIFH----- 361
 Db 332 CYGPVRSVLYDLAS--VDSC-----EENSLEIIFH----- 361
 QY 678 -----LASFYMDNCTEKSKEEDTSOYVAFEEFDLDTYMMRCVSDDGTTGQOLI 726
 Db 678 -----LASFYMDNCTEKSKEEDTSOYVAFEEFDLDTYMMRCVSDDGTTGQOLI 726
 QY 362 -CKSPH-----RHRMVL-----EPLINK-LIQAKNDL 387
 Db 362 -CKSPH-----RHRMVL-----EPLINK-LIQAKNDL 387
 QY 727 GCKSAVDEDPKLEKDAOSYASNYDRVKYHPLKLMADAELKHLNPLSKALLKYKNRL 786
 Db 727 GCKSAVDEDPKLEKDAOSYASNYDRVKYHPLKLMADAELKHLNPLSKALLKYKNRL 786
 QY 388 -IPKEFLNFNLQIYMFLETFAYHOPTL-----KQOAPHLKAEGNS 430
 Db 388 -IPKEFLNFNLQIYMFLETFAYHOPTL-----KQOAPHLKAEGNS 430
 QY 787 GRPMYMFALFMVLFVLSLQVVRHTKAPYNTWNEESYDSEYFDENETCPPOINTTKPD- 845
 Db 787 GRPMYMFALFMVLFVLSLQVVRHTKAPYNTWNEESYDSEYFDENETCPPOINTTKPD- 845
 QY 431 MLITGHILLLGGIYLGVQLWFRRHFI-WISPLDSYFELIFLFO-ALLVVSVQL 487
 Db 431 MLITGHILLLGGIYLGVQLWFRRHFI-WISPLDSYFELIFLFO-ALLVVSVQL 487
 QY 846 -WVLDLQSTKYTGOMYWGYPPLSFACTNQVDFCFLRLRAMKADPNMP---DTNGNTV 291
 Db 846 -WVLDLQSTKYTGOMYWGYPPLSFACTNQVDFCFLRLRAMKADPNMP---DTNGNTV 291

QY 488 CF---LAIEWLPPLVSALVGLWNLILYTRGFOHTGIVSMIQKVLRLRFLFLYL 543
 Db 900 CSATSGVRQQNQWILALCITFFGWINLFLMTRKMPRFGIVVMFDIV-KTFERFPVFV 958
 QY 544 VFLFGGAVALVISLSQFAWRPAPT--GPNTATESKOPMEOSEDEENGQAQRLLEASLEL 600
 Db 959 LFIAFQFSSSFVWILON--RPEFSTIFMSPLKTTVW--MIGB----- 995
 QY 601 FKFTIGMGEALFQEQHFRGM----VLLIAVLYLTYILLNLMLMSSETVNSV 652
 Db 996 FEFT--GIEFGDETHAEGPAHTAVACALEFFFCIMTLLMNLVLAGVDIKGV 1052
 QY 653 ATDSWSWTWKLOKAIS-VLEME-----NGY--WCRKK 681
 Db 1053 -QEKAELKLRLAMQDVLYQIEASLHFIQIYKATCRYATFPYCKLHKTGAGWSNFR 1111
 QY 682 ORGAVMLTVGRKPD 695
 Db 1112 RRFG--LSVSTDPE 1123

RESULT 8

JH0588 calmodulin-binding protein trpl - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
 C;Accession: JH0588
 R;Phillips, A.M.; Bull, A.; Kelly, L.E.
 Neuron 8, 631-642, 1992
 A;Title: Identification of a *Drosophila* gene encoding a calmodulin-binding protein with
 A;Reference number: JH0588; MUID:92232293
 A;Accession: JH0588
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1124 <PHI>
 A;Cross-references: GB:MB8185; NID:9469057; PID:9158715
 A;Experimental source: head
 C;Genetics:
 A;Gene: trpl
 A;Cross-references: FlyBase:FBgn0005614
 C;Keywords: calmodulin binding; phosphoprotein; transmembrane protein
 F;341-362;/domain: transmembrane #status predicted <TM1>
 F;374-395;/domain: transmembrane #status predicted <TM2>
 F;512-533;/domain: transmembrane #status predicted <TM4>
 F;549-572;/domain: transmembrane #status predicted <TM5>
 F;643-668;/domain: transmembrane #status predicted <TM6>
 F;710-727;809-815;/Region: calmodulin binding #status predicted
 F;722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.9%; Score 197.5; DB 2; Length 1124;
 Best Local Similarity 19.7%; Pred. No. 5.8e-07;
 Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

QY 131 VNACTIPLQLQIDRSQNQPL-----VNQCTDD 159
 Db 25 VGGCCVPL-----GLPQPLLERKKFLAVERSDMPNVRILQKHLINNCMDP 77

QY 160 YYRGHSALHATEKRSIQCQKLLVING----ANTHARAC-----GPFQKG 201
 Db 78 L--GRRALTAIDNELEMVLLVVMGVTKDALLHAINAEFVEAVELLEHEELLYKE 135

QY 202 Q-----GTCFVGFEL_PLSLACTKQMDVSYLLEN-----PH-----QPAL 238
 Db 136 EPYSWQKVQDINTAMFAPDITPLMLAAHKNFIELRILDRGAAYVYPHDITRCGCECVRL 195

Query Match 4.8%; Score 191; DB 2; Length 1274;
 Best Local Similarity 20.2%; Pred. No. 2.2e-06;
 Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;

Db 196 TAEDSLRHSLSRVNYRALGSPSLCLTSNDPSAFQLSWELRLVALTEQECSEYMDL 255

QY 289 IRNLO---DLTPLKLAKEGKIEI-----FRHILQREFSGLHSLSRKFTWC 332

Db 256 RQOCQKFADLIDQRTSNEHAIINYPDQMSSEPGDRMSLTRLVQASYKQKKFV-A 313
 QY 333 YGPVRVSL---YDASVDSCEENSYLETAFHCKSPHRURMVTEPLNKL-----QAK 383
 Db 314 HSNIQOLSSSIWWD-GLPSEFRKSIVDKVIT-CIA---QVAVIPLKICLIVCAPNR 365
 QY 384 WLILPKFKFLFLCN---LJYMFIFTAVA-----YHOPLTKKGAAPHKAEVG 429
 Db 366 TQQLMRKPFMKFLIHASSYLFLEFLILVQSQRADDFFVRIFTTRMKKELAEOLRQG 425
 QY 430 SMLTCIHLILGGYLVQGLWYFWRRIWISRIDSEFEELFOALL-TWVSOL 487
 Db 426 ---TPSKLELIUVMV---IGFWEEVBIFAVGMKSYLRNMWNFDFLRLNSLYVSM 477

QY 488 OFLAIW-----YLP-----LVSALVLGWNLLYTRGFQ 518

Db 478 CUFRAVYIQTATEARDPOMAYPRKWHBPDQPLIAEGLFVANFSALKLWHFSIP 537

QY 519 HNGIVSVMIQVILRDLRFLILYVFLFGPAVALVLSQEW-----RPEAPTPGNAT 572

Db 538 HLGPOLOSLGRKVI-DIVKFFIYIYLVLFR-A---CGLNOLWLFAALEKSKCIVLPG- 591

QY 573 ESVQPEQEGEDEGNA-----QYRGLIASLFLKFTIGMEL-----AEEQLHFR 619

Db 592 -----GEADWGSQHDSCKMWRQFNGLFEQSLSLWASFGVGMVGLDFELSGIKSYTRFW 644

QY 620 GMVLLILAYLTYILLNLMLALMSSETVNSVATDSWSIKLQKAISVLEMEYWWCR 679

Db 645 G-LMFGSASVIVNVLAMMSNSYAMIDHSHTDWKAR-----IKLMSVY 694

QY 680 KRQRAVMLTVGTPDCSPDERWCFRV-----EVNNWASWEQPLPTLC 722

Db 695 FEDSA---TIPPPFNVLPSWKWIRIFRKSKTDQRSKKRKEQEOFSEYDINMSLV 750

QY 723 EDPSAGVPRLENPLASPKED-E-GASSEENYVPUQOLQ 762

Db 751 W-RVYAMHRFEN---NPVSEDDINEVKSEINTMYEME 787

RESULT 9

JN0015 trp protein - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 07-Sep-1990 #sequence_revision 07-sep-1990 #text_change 02-Feb-2001
 C;Accession: JN0015
 R;Wong, F.; Schaefer, E.L.; Roop, B.C.; Lamendola, J.N.; Johnson-Seaton, D.; Shao, D.
 Neuron 3, 81-94, 1989
 A;Title: Proper function of the *Drosophila* trp gene product during pupal development
 A;Reference number: JN0015; MUID:90148782
 A;Accession: JN0015
 A;Molecule type: mRNA
 A;Residues: 1-1274 <WON>
 C;Comment: This photoreceptor membrane-associated protein is not required for the occ
 C;Genetics:
 A;Gene: trp
 A;Cross-references: FlyBase:FBgn0003861
 A;Map position: 99C5-6
 C;Superfamily: TRPC3 protein
 C;Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane P
 F;1257-1263;/Region: nucleotide-binding motif A (P-loop)
 F;64,70,899;/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;191,602,880,883,924;/Binding site: phosphate (Ser) (covalent) #status predicted
 F;800,1266;/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 4.8%; Score 191; DB 2; Length 1274;
 Best Local Similarity 20.2%; Pred. No. 2.2e-06;
 Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;

Db 153 NAQCTDYYKGSALMAIEKRSLOCVKLIVENGANHARACGRFQOKSGGCFYFGEPL 212

Db 62 NINCTDPMR--SALTSATENENFDLMLVILEHNIEV-----GDALLHAISEY 108

QY 213 LSLACTKQWDVSYLLENPHQASLQATDSQNT----VHALMISDNASENIALVTS 268
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 109 VEAVEELLQWETNH--KEGQPYSEBEAVDRSKSTFTVDITFLIAHRNNYEIKI-- 162
 C;Species: Drosophila melanogaster
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
 C;Accession: JU0092
 R;Montell, C.; Rubin, G.M.
 Neuron 2, 1313-1323, 1989
 A;Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
 A;Reference number: JU0092; MUID:90180449
 A;Accession: JU0092
 A;Molecule type: mRNA
 A;Residues: 1-1275 <MON>
 A;Experimental source: strain Oregon R
 C;Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the pr
 C;Geometrics:
 A;Gene: trp
 A;Cross-references: FlyBase:FBgn0003861
 C;Superfamily: TRPC3 protein
 C;Keywords: transmembrane protein
 F;330-354-/domain: transmembrane #status predicted <TM>
 F;415-436-/domain: transmembrane #status predicted <TM>
 F;455-471-/domain: transmembrane #status predicted <TM>
 F;505-527-/domain: transmembrane #status predicted <TM>
 F;612-630-/domain: transmembrane #status predicted <TM>
 F;636-661-/domain: transmembrane #status predicted <TM>

QY 269 MYDGILQAGARL--CPTVQLEDE-INTLQDITPLKIAKEG 305
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 163 ---LIDRGATLPMHDVKCCDECCTSQTDSLRSQSRTNAYRALSASSLIALSSRDP 218
 306 KIEFRHILQREFSGISHLRSRKFTENCYGPVRVSLYLAS--VDSCEENSVELTIAFHCK 363
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 219 VLTAFQ--LSWEILKIQAMESEFRAE-YTEMQRMQDFGTSLLDARTSMELLEVMLNFH 275
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 QY 364 SP-----HRHMVLEP-LNKLQAKWDLIPF----- 391
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 276 EPHSIWICLASSETLERIKLAIRYKOTFVAHPNVOQLLAIWYGLPGPQEASQQLMD 335
 392 FLNFLCNL-TMVFITAVAVYHPTKKAAPHLK AEVGNSMLIG-----HILL 441
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 336 VVKLGCSFPPIY-----SKYKILAPDSEGAKFMRNPLSSSSRTPCSYMFLLML 383
 442 GGIYLVLQGQ-----WTF-----WRRH----- 460
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 384 GAASLRVQVTFELAAPPWMITMLEDWRKHTGRSLPGPIELAITYYMALEFEELKSLYS 443
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 QY 461 -----IW-ISPIDSFEILFLP-QALLTVSQVLQFLATEWL-----PL 498
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 444 DGLFEYIMDLMNIVDYNISNMVYWTWILCRATAWIVHLDWFRGDPYFREHWHPFDPM 503
 499 LVS-----ALVLGWNLYTYTRGFOHTGYISVMIQTKVTLRDLRFLTYLVFLGFAVA 552
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 504 LLSEGAFAAGAVFSTKLVHFINSNPHLGLQVSLGMRMI-DIKEFFIYTIVLVEAFLG- 560
 553 LVSLQEAWRPEAPTPGNATESVOMEGOEDDEGNA-----QYRGLLEASLELFPTIGM 607
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 561 -CGLNOLWV-YAEELKNKCYHLHPDAVDDQEKACTWRFSLNFSLFTOSLFWASGL 618
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 QY 608 GELAFQE---QLHFRGMVLLLAVALTYTILLNMLIAMSETVNSVATDSMSIWKLO 663
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 619 VDLVSDFDLAGIKSFTRFWALMLFGSYSVINIVLNLAMMSNSYQIISERADTEWKFA 678
 QY 664 KA 665
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 679 RS 680
 RESULT 10
 JU0092
 trp protein - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
 C;Accession: JU0092
 R;Montell, C.; Rubin, G.M.
 Neuron 2, 1313-1323, 1989
 A;Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
 A;Reference number: JU0092; MUID:90180449
 A;Accession: JU0092
 A;Molecule type: mRNA
 A;Residues: 1-1275 <MON>
 A;Experimental source: strain Oregon R
 C;Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the pr
 C;Geometrics:
 A;Gene: trp
 A;Cross-references: FlyBase:FBgn0003861
 C;Superfamily: TRPC3 protein
 C;Keywords: transmembrane protein
 F;330-354-/domain: transmembrane #status predicted <TM>
 F;415-436-/domain: transmembrane #status predicted <TM>
 F;455-471-/domain: transmembrane #status predicted <TM>
 F;505-527-/domain: transmembrane #status predicted <TM>
 F;612-630-/domain: transmembrane #status predicted <TM>
 F;636-661-/domain: transmembrane #status predicted <TM>

Query Match 4.8%; Score 190.5; DB 2; Length 1275;
 Best Local Similarity 19.9%; Pred. No. 2.4e-06;
 Matches 130; Conservative 98; Mismatches 253; Indels 171; Gaps 27;

QY 153 NQCTDDYXRGSHSALTAERSLOCVKLIVENANGANVHARACGRPFQKGOTCTYFGELP 212
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 62 NINCIDPMNR-SALISAIENENFDNVILLEHNTEV-----GDALLHAISEY 108
 213 LSLACTKQWDVSYLLENPHQASLQATDSQNTV--LHALMISDNASENIALVTS 269
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 109 VEAVEELLQWETNH--KEGQPYSEBEAVDRSKSTFTVDITPLLAHRNNYEIKI-- 162
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 QY 270 YDGQIAGARL-----CPTVQLEDE-INTLQDITPLKIAKEG 306
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 163 ---LIDRGATLPMHDVKCCDECCTSQTDSLRSQSRTNAYRALSASSLIALSSRDP 219
 307 IEFRIILQREFSGISHLRSRKFTENCYGPVRVSLYLAS--VDSCEENSVELTIAFHCKS 364
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 220 ITAFO--LSWEILKIQAMESEFRAE-YTEMQRMQDFGTSLLDARTSMELLEVMLNHE 276
 QY 365 P-----HRHMVLEP-LNKLQAKWDLIPF----- 391
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 277 PSHDWICLGORQTLERIKLAIRYKOTFVAHPNVOQLLAIWYDGLPGFRRKQASQQLMD 336
 392 FLNFLCNLTYMIFAVAVYHPTKKAAPHLKAEVGNSMLIGTCHILILUGITLVGOL 451
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 337 VWKLGCSPFPISKYLAPDSEGAKFMRKPKFVFKITHSCSYM--FPLMLIIGAASLRVVOI 394
 QY 452 -----WTF-----WRRH----- 461
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 395 TFELLAFFPWNMTMLEDWRKHTGRSLPGPIELAITYYMALEFEELKSLYSGLFEYIMD 454
 QY 462 W-ISPIDSFEILFLP-QALLTVSQVLQFLATEWL-----PLIVS-----A 502
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 455 WNTDVYISHNHYVWTLCRATWIVHLDWFRGDPYFREHWHPFDPMBSGAGAAG 514
 QY 503 DVLGWNLTYTYTRGFOHTGYISVMIQTKVTLRDLRFLTYLVFLGFAVALLSISQEAR 562
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 515 MVFSVSLKLVHFINSNPHLGLQVSLGMRMI-DIKEFFIYTIVLVEAFLG--CGLNQLLW 570
 QY 563 PEAPTPGNATESVOMEGOEDDEGNA-----QYRGLLEASLELFPTIGMELAFQE-- 614
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 571 -YAEELKNKCYHLHPDAVDDQEKACTWRFSLNFSLFTOSLFWASGLVLDLVSFDLAG 629
 QY 615 -QLHFRGMVLLLAVALTYTILLNMLIAMSETVNSVATDSMSIWKLOA 665
 ; || : || : || : || : || : || : || : || : || : || : || : || : || : || : || :
 Db 630 IKSFTFWALMLFGSYSVINIVLNLAMMSNSYQIISERADTEWKFA 681
 RESULT 11
 I38361
 TRPC1 protein - human
 C;Species: Homo sapiens (man)
 C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
 C;Accession: I38361
 R;wes, P.D.; Chevastich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
 Proc. Natl. Acad. Sci. U. S. A., 96(22), 9652-9656, 1999
 A;Title: TRPC1, a human homolog of a Drosophila store-operated channel.
 A;Reference number: I38361; MUID:96003837
 A;Accession: I38361
 A;Molecule type: mRNA
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Cross-references: EMBL:X89066; NID:91019786; PID:91019787
 C;Superfamily: TRPC3 protein
 C;Keywords: transmembrane protein
 F;370-404-/domain: transmembrane #status predicted <TM>
 F;415-436-/domain: transmembrane #status predicted <TM>
 F;455-471-/domain: transmembrane #status predicted <TM>
 F;505-527-/domain: transmembrane #status predicted <TM>
 F;612-630-/domain: transmembrane #status predicted <TM>
 F;636-661-/domain: transmembrane #status predicted <TM>

Query Match 4.3%; Score 174; DB 2; Length 810;
 Best Local Similarity 19.1%; Pred. No. 2.5e-05;
 Matches 139; Conservative 116; Mismatches 244; Indels 228; Gaps 33;

Qy 86 GVPEDLAGPEY-----LSKSKYLTSETEVGSTCKTCIMKAV----- 124
 Db 37 GAPPSPGLPPSWAMMAALYPLSTDGLSGASSSSPSSSPNEMALKDREVKEENT 96

Qy 125 LNLKGDFVNAC-----IPLQLIDDSGPNQPLVNAQCTDDYRGRHSALHATEKRSIQ 177
 Db 97 LNEKIFLLACDKGYVMVKILE-ENSSGD----LNINCVD--VLGRNAVTITENELD 149

Qy 178 CVKLILVENGANVHARACGRFFQKOGTCTF--YFGELPLSLAACTKWDVVSYLIE---- 230
 Db 150 ILQLLDYG-----COKLMERTONPEYTTMDWAPVILAHHNNYEILTMLLKQDVSL 202

Qy 231 -NPH-----IPLQLIDDSGPNQPL-----QASLQATDSQGIVLHALVMISD 257
 Db 203 PKPHAVGCECTLCASKKKNDLSLRHSRFLRDYLTVCLASPALIMITE--DPILRAFELSAD 260

Qy 258 -----NSAENIALVTSWMDGLIQAQARLCPYQLEDTIN----- 291
 Db 261 LKELSLVVEFNRNDYEEALAROCKHAKDILQAQR--NSRELEVENTHISDEPKDKGIL 318

Qy 292 --LQDTPKLAKEKGKIEFRHLQREFSGLSHLSRKFTEWCYGPVRVSLYDLSAVDSC 349
 Db 319 EERMUNSLRKLAIKN-----QKEF----- 344

Qy 350 EENSVLTEIIFHCCKSPHR-----MUVLE----PLKL-----QKWDLIPKFL 393
 Db 345 QQ--FLNTVWFGQMGSYRKPCTKKIMTVLTVGFPVLSCLYTLAPSQFGRHTPME 402

Qy 394 NFLCNLIMLYMIFT-----AVAYHOPTKKQOAPHKAEVGNMSMLTGHLILIGGIYL 447
 Db 403 KFIIGAGASYTFLLINLYSLVYNEKD-----KNTMGPALERIDYLIL-----WI 448

Qy 448 VQOLMWFWRHVFTMISFIDSYF-----ILFLFQA-LLTVVSQVLCFLAT-----E 493
 Db 449 IGMWSDIKR--LWEGLEDFLEESRNOLSFVANSLYLATFALKVVAHKFRDEADRKD 505

Qy 494 W-YPLVLYSALVIGLWNLNYYTGFQHGTGISTS-----IOKVTLRDLRFLLYLYL 546
 Db 506 WDAFFPLTYAEGLFRFANVLYSLRLFFMTTSSILGPLOISMGMQLQDFGKFLGMFLVL 565

Qy 547 FGFIAVALVLSOEARWPEAPTGPNTAEVOPMEOQEDEGNGAQYRRGILEASLEFIFTG 606
 Db 566 FSFTIGLTYODKSY-----TSKECKDCVGIFCBOQSNDT--FHISFTGTCFAFWYIFS 617

Qy 607 MGEIAF-----EQQLHFRGMVMLILLAYLVLLYILLNMLTALEMSEVNSVATDSWS 658
 Db 618 LAHWVIAFVTRFSYGEELQSFVGAV--IVGTYNWVIVLTKLVLHKSQFOLIANHEDK 675

Qy 659 IWKICKA 665
 Db 676 EWKFARRA 682

C; Superfamily: syphilis spirochete probable ankyrin; ankyrin repeat homology
 F; 281-313/Domain: ankyrin repeat homology <AN22>

Query Match 4 2%; Score 167.5; DB 1; Length 934;
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 76 RDRLFNAVSRGVPEPDLAGLPEYLSKTSKLTDSYESTGKTCMLKAVLN----- 126
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 448 RDPLHVAVSRRAHLDIV---KFLFREPQKM---IARDINGNTLHYAVANDDRAVERFL 500
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 501 MREGADIFSTNVHGVSPVSLTATTSGGREDWILTAANVHAOTRG---GNTPLHPLACEWKM 556
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 557 LTQATINGILRKGAIEARNHQ-----ETPLFSAVKSANEAVISTLHPQAG 603
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 234 QPASLQATDSQGNTVHALVMISDNAENIALVTSWMDGLIQAQARLCPYQLEDTINQ 293
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 604 NPALVADARAWGNTVHLACVRSALRSADVL-----IREADAR--HVSILNARNLS 652
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 294 DLTPKLAKEKGKIEFRHL 314
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

Query Match 653 GKPPPLHAAARGNYDFIRLLL 673
 Best Local Similarity 27.6%; Pred. No. 9.7e-05; Mismatches 95; Indels 57; Gaps 10;
 Matches 72; Conservative 37; MisMatches 95; Indels 57; Gaps 10;

RESULT 13
 T23729
 Hypothetical protein M05B5.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T23729
 R;Gardner, A.
 submitted to the EMBL Data Library, April 1996
 A;Reference number: Z19790
 A;Accession: T23729
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-481 <WFL>
 A;Cross-references: EMBL:Z71265; PIDN:CAA95836.1; GSPDB:GN00019; CESP:M05B5.6
 A;Experimental source: clone M05B5
 C;Genetics:
 A;Gene: CESP:M05B5.6
 A;Map position: 1
 A;Introns: 50/2; 99/1; 133/3; 185/3; 229/3; 402/3; 457/3

Query Match 291 NLQDQITPLKIAKGGKIELFRHILOREFSGLHSRSKFTEWCGPVRYSLYDLSAVDSC 350
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;
 Matches 90; Conservative 58; MisMatches 149; Indels 95; Gaps 17;

Query Match 57 NWKELKLKLSGKKG---VIRH-----VPILYVNOKLIDCAFFY-- 94
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 351 ENSVLEIIFAHCKSPHRHMVLEPLNKLUQKMDLLPKFFLNFCLNLIYMFIFTAVY 410
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 411 HOPTLKQOAPHKAEVGNMSMLGHTLILLGGIYLVLGOLWWFRRHFEWISFIDSYF 470
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 131 MFLVLTGK-----IKARITKS-VSTWFLIVAFCFNIFTYMATLAVWLPLV-----GYDDYHL 182
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 471 EIEFLFOALITWVSVQVLCFLAIEWYPLVLVSALVLGWMILLYTGRFHGTGIVSMIOV 530
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 183 EVKKT-----VTFNPLII-----ATISAWANALLYINRK-SPPGIVTFMMTR 222
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

Query Match 531 ILRDLRFLILYVLFLEGAVLVSQBARWPEAPTGPNTS-----VOPMEOQEDEGC 587
 Best Local Similarity 23.0%; Pred. No. 0.00024; Mismatches 149; Indels 95; Gaps 17;

RESULT 12
 H71274
 probable ankyrin - syphilis spirochete
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: H71274
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwintz, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDavid, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science, 281, 375-388, 1998
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; MUID:98332770
 A;Accession: H71274
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-934 <COL>
 A;Cross-references: GB:AE001254; GB:AE000520; NID:93323148; PIDN:AAC65803.1; PID:9332314
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0835
 C;Gene: TP0835

RESULT 14

T13940

Ankyrin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000

C;Accession: T13940

R;Dubreuil, R.R.; Yu, J.

Proc. Natl. Acad. Sci. U.S.A. 91: 10285-10289, 1994

A;Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosophila. Reference number: Z17820; MUID:95024098

A;Accession: T13940

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-1549 <dub>

A;Cross-references: EMBL:135601; NID:9557083; PID:9557084; PIDN: AAC37208.1

A;Cross-references: FlyBase:FBgn0011747

Query Match 3.9%; Score 157; DB 2; Length 1549; Best Local Similarity 22.8%; Pred. No. 0.0013; Matches 91; Conservative 61; Mismatches 134; Indels 114; Gaps 17; Query 101 TSKYLTSEYTGGTSGKQCLMKAVNLKDGVNACILPLQIDRDSGNPQPLVNAQCTDY 160 Db 363 TVDYLT-ALKVAACGHVVKVAKLILDDYKANPNAR----- 397

Qy 161 YRGHSALHIAIERKLSQLCVKLLVENGAWHARACGRF-----FQKGQGTCYF---- 208 Db 398 -NGFTPPLHACKKNRKRAVEELLIKHGANGATGATTEGSLPLHVASFPMGCTINTIVYLLHEA 456

Qy 209 -----GELPLSLAETKOMWVSYLLENPHOPASLQATDSQGNTVHLALWMSDNA 260 Db 457 SADLPTIRGETPLHLAAARNQADITIILRS-----AKYDAIVREGQTPLHVAERLUG---- 508

Qy 261 ENALVTSMYDGLIQAQARLCPTVOLEDIRNLQDLTPLPKLAKEKGKIEFRHTIQ---- 315 Db 509 -NINIIML---LLQHGREI-----NQSNDKYSALHIAAREQENIVQVLLENGAE 556

Qy 316 -----REFGGLSHLSRKTEWCVGPVRVSYLDIASVDSCEENSVLET-IAFHCKSPHRHR 369 Db 557 NAVTKKGFTPL-HLACKYK-ONVQVILLQNGASIDFOGKNDTPHLVATHYNNSPTE 613

Qy 370 MYVLEPLKKLQQKWDLILPKFLNFLCNLIMLYMFITAVAYHOPTL---KKOAP-HLK 424 Db 614 LLIKNGSSSPNLCAR---NGQCAIHACKKNYLEIAMQULLQHQGADVNTISKSGFSPLHLA 669

Qy 425 AEVGN---SMLI-----TGHILL 439

Qy 670 AOGGNVNDMVKVQLLEYGVISAAKNGLTFLHVAQEGHVLV 709

RESULT 15

T42714

Ankyrin 3, splice form 2 - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000

C;Accession: T42714

R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.

J. Cell Biol. 130, 313-330, 1995

A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.

A;Reference number: Z22237; MUID:95340633

A;Keywords: ankyrin; ankyrin repeat homology

Query Match 3.8%; Score 151; DB 2; Length 1765; Best Local Similarity 27.7%; Pred. No. 0.0044; Matches 78; Conservative 43; Mismatches 91; Indels 70; Gaps 1

Qy 162 RGHSALHIAIERKLSQLCVKLLVENGAWHARACGRFQKGQGTCYFGEGLSLAETKQ 221 Db 448 RGETAHMARSQGAEVRYVQDGQVEAKA----KDDQT-----PLHSARLGK 494

Qy 222 WDVVSYLLENPHOPASLQATDSQGNTVHLALWMSDNAEINALVATMSYMDGILQCARLC 281 Db 495 ADIVQQLQ--QGASPNAATTSQGTPHL--LAKREGHEDVAAT-----LLDRIASLS 542

Qy 282 PTWQLEDFIRDINQDPLPLKLAKEKGKIEFRHTILQRFFS---GISHLSRKTEWCVGPVR 337 Db 543 ITTK-----KGFTPPLHVAACYGKLEVASSLQLQSASPDAGKSGLT-----PLH 586

Qy 338 VSLYLASVSDSCEENSVLETIAFHCKSPHRHMVILEPLNKLUOKWDLIPKFELNLC 397 Db 587 VAAH-----YDNOKVALLIDDOASPHAAKNGYTPHL--IAAK-----KNOMDIAT 631

Qy 398 NLI-YMFIFTAVAYHOPTLKKQAAPIHLKAEGVN---SMLIT 434 Db 632 SLLEGADAVY---TROGIASVILAQEGHYDVISLIS 668

Search completed: July 18, 2001, 15:59:29
Job time: 162 sec

Thur Oct 18 15:25:10 2001

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